



## lalign output for SEQ ID 2 vs. SEQ ID 14

[ISREC-Server] Date: Tue Jan 25 17:25:30 Europe/Zurich 2005

LALIGN finds the best local alignments between two sequences version 2.0u66 September 1998 Please cite: X. Huang and W. Miller (1991) Adv. Appl. Math. 12:373-381

### Comparison of:

(A) ./wwtmp/lalign/.18855.1.seq SEQ ID 2  
(B) ./wwtmp/lalign/.18855.2.seq SEQ ID 14  
using matrix file: BL50, gap penalties: -14/-4

61.1% identity in 108 aa overlap; score: 456 E(10,000): 7.4e-34

	10	20	30	40	50	60
SEQ	LHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSPRMEPIITND					
	20	30	40	50	60	70
SEQ	LTASGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSLTTQGPPIITNN					
	70	80	90	100	110	
SEQ	RFTSQRYDQGGNFTSEMIIHNVEPSDSDGNIRCSLQNSRLHGSAYLTVQ					
	80	90	100	110	120	
SEQ	RFTYASYNSTDSDFISELIHDVQPSDGSVQCSLQNSHGFSAFLSVQ					

53.3% identity in 92 aa overlap; score: 290 E(10,000): 4.5e-19

	300	310	320	330	340	350
SEQ	KKSEKEKTNK--ETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSCGPPH					
	.. :: . . . . .	:: . . . . .	:: . . . . .	:: . . . . .	:: . . . . .	..
SEQ	RKSANMRTNKADPETKLKGKENVGYSSDEAKAAQTASLPPKSAEVSLPEKRSSL--PY					
	140	150	160	170	180	190
	360	370	380			
SEQ	QRADQRPPRPASHPQASFNLASPEKVSNTTVV					
	.. . . . .	:: . . . . .	:: . . . . .			
SEQ	QELNKHQPGPATHPRVSDIAPQKVRNVTLV					
	200	210	220			

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**lalign output for SEQ ID 4 vs. SEQ ID 14**

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Comparison of:

(A) ./wwtmp/lalign/.19190.1.seq SEQ ID 4  
(B) ./wwtmp/lalign/.19190.2.seq SEQ ID 14  
using matrix file: BL50, gap penalties: -14/-4

61.0% identity in 105 aa overlap; score: 447 E(10,000): 4.8e-33

	20	30	40	50	60	70
SEQ	SGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSPRMEPIITNDRFT					
	::::	.....	:::	.....	.....	.....
SEQ	SGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWKLLMWTLNQMVVLSTTQGPIITNNRFT					
	30	40	50	60	70	80
	80	90	100	110		
SEQ	SQRYDQGGNFTSEMMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQ					
	...	..	.....	.....	.....	.....
SEQ	YASYNSTDSDFISELIIHDVQPSDGSVQCSLQNSHGFSAFLSVQ					
	90	100	110	120		

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53.3% identity in 92 aa overlap; score: 290 E(10,000): 4.5e-19

	300	310	320	330	340	350
SEQ	KKSEKEKTNK--	ETETESEN	GYNSDEQKTTDTASLPPKSC	CESSDPEQRN	SSCGPPH	
	..	..	..	..	..	..
SEQ	RKSANMRTNKADP	EKTNKADP	EKTNKADP	EKTNKADP	EKTNKADP	EKTNKADP
	140	150	160	170	180	190
	360	370	380			
SEQ	QRADQRPPR	PASHPQ	QASFN	ASPEKVS	NTTVV	
	..	..	..	..	..	..
SEQ	QELNKHQPGP	ATHPRV	SFDIASPQKV	RNVTLV		
	200	210	220			

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## lalign output for SEQ ID 6 vs. SEQ ID 14

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Comparison of:

(A) ./wwtmp/lalign/.19757.1.seq SEQ ID 6  
(B) ./wwtmp/lalign/.19757.2.seq SEQ ID 14  
using matrix file: BL50, gap penalties: -14/-4

57.9% identity in 114 aa overlap; score: 458 E(10,000): 5e-34

	10	20	30	40	50	60
SEQ	LLTVPEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSPRME					
	..	..	..	..	..	..
SEQ	LVILAQLTASGSSYQIIEGPQNVTVLKDSEAHFNCTVTHGWLKLLMWTLNQMVVLSSLTTQG					
	20	30	40	50	60	70
	70	80	90	100	110	
SEQ	PIITNDRFTSQRYDQGGNFTSEMIHNVEPSDGSNIRCSLQNSRLHGSAYLTVQ					
	..	..	..	..	..	..
SEQ	PIITNNRFTYASYNSTDSDFISELIIHDVQPSDGSVQCSLQNSHGFSAFLSVQ					
	80	90	100	110	120	

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53.3% identity in 92 aa overlap; score: 292 E(10,000): 3e-19

	300	310	320	330	340	350
SEQ	KKSEKEKTNK---	ETETESGNENSGYNSDEQKTETASLPPKSCESSDPEQRNSSCGPPH				
	..	..	..	..	..	..
SEQ	RKSANMRTNKADPETKLKGKENYGYSSDEAKAAQTASLPPKSAEVSLPEKRSSL--PY					
	140	150	160	170	180	190
	360	370	380			
SEQ	QRADQRPPRPASHPQASFNLASPEKVSNTTVV					
	..	..	..	..	..	..
SEQ	QELNKHQPGPATHPRVSFDIASPKVRNVTLV					
	200	210	220			

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